

266811US0XPCT.ST25  
SEQUENCE LISTING

<110> May, Oliver  
Buchholz, Stefan  
Schwarm, Michael  
Drauz, Karlheinz  
Turner, Robert  
Fotheringham, Ian

<120> MUTANTS FOR THE PREPARATION OF D-AMINO ACIDS

<130> 266811US0XPCT

<140> 10/527,061

<141> 2005-03-09

<150> PCT/EP03/11432

<151> 2003-10-15

<150> DE 102 51 184.5

<151> 2002-11-04

<160> 8

<170> PatentIn version 3.3

<210> 1

<211> 948

<212> DNA

<213> Arthrobacter crystallopoietes

<220>

<221> CDS

<222> (1)..(948)

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agt tcg gaa tca aga ccc gaa gtc gtc gcc cgc ttg att gcc ctg ctg	96
Ser Ser Glu Ser Arg Pro Glu Val Val Ala Arg Leu Ile Ala Leu Leu	
20 25 30	
gaa gaa gca gct tcc cag ggc gcg gaa ctg gtg gtc ttt ccc gaa ctc	144
Glu Glu Ala Ala Ser Gln Gly Ala Glu Leu Val Val Phe Pro Glu Leu	
35 40 45	
acg ctg acc acg ttc ttc ccg cgt acc tgg ttc gaa gaa ggc gac ttc	192
Thr Leu Thr Thr Phe Phe Pro Arg Thr Trp Phe Glu Glu Gly Asp Phe	
50 55 60	
gag gaa tac ttc gat aaa tcc atg ccc aat gac gac gtc gcg ccc ctt	240
Glu Glu Tyr Phe Asp Lys Ser Met Pro Asn Asp Asp Val Ala Pro Leu	
65 70 75 80	
ttc gaa cgc gcc aaa gac ctt ggc gtg ggc ttc tac ctc gga tac gcg	288
Phe Glu Arg Ala Lys Asp Leu Gly Val Gly Phe Tyr Leu Gly Tyr Ala	
85 90 95	
gaa ctg acc agt gat gag aag cgg tac aac aca tca att ctg gtg aac	336
Glu Leu Thr Ser Asp Glu Lys Arg Tyr Asn Thr Ser Ile Leu Val Asn	
100 105 110	
aag cac ggc gac atc gtc ggc aag tac cgc aag atg cat ctg ccg ggc	384
Lys His Gly Asp Ile Val Gly Lys Tyr Arg Lys Met His Leu Pro Gly	
115 120 125	

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cac His	gcc Ala	gat Asp	aac Asn	cgg Arg	gaa Glu	gga Gly	cta Leu	ccc Pro	aac Asn	cag Gln	cac His	ctt Leu	gaa Glu	aag Lys	aaa Lys	432
130						135					140					
tac Tyr	ttc Phe	cgc Arg	gaa Glu	gga Gly	gat Asp	ctc Leu	gga Gly	ttc Phe	ggt Gly	gtc Val	ttc Phe	gac Asp	ttc Phe	cac His	ggc Gly	480
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gtg Val	cag Gln	gtc Val	gga Gly	atg Met	tgt Cys	ctc Leu	tgc Cys	aac Asn	gac Asp	cgg Arg	cga Arg	tgg Trp	ccg Pro	gag Glu	gtc Val	528
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tac Tyr	cgc Arg	tct Ser	ttg Leu	gcc Ala	ctg Leu	cag Gln	gga Gly	gca Ala	gag Glu	ctc Leu	gtc Val	gtc Val	ctg Leu	ggc Gly	tac Tyr	576
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aac Asn	acc Thr	ccc Pro	gat Asp	ttc Phe	gtt Val	ccc Pro	ggc Gly	tgg Trp	cag Gln	gaa Glu	gag Glu	cct Pro	cac His	gcg Ala	aag Lys	624
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aaa Lys	gca Ala	gcc Ala	ggc Gly	gag Glu	ggc Gly	gat Asp	gaa Glu	gtc Val	gtc Val	gtt Val	gtg Val	aaa Lys	gca Ala	gac Asp	atc Ile	816
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gac Asp	atg Met	ggc Gly	aag Lys	ccc Pro	tat Tyr	aag Lys	gaa Glu	agc Ser	gtc Val	ttc Phe	gac Asp	ttc Phe	gcc Ala	gcc Ala	cat His	864
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cgg Arg	cgc Arg	ccc Pro	gac Asp	gca Ala	tac Tyr	ggc Gly	atc Ile	atc Ile	gcc Ala	gaa Glu	agg Arg	aaa Lys	ggg Gly	cgg Arg	ggc Gly	912
	290					295					300					
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Glu Glu Ala Ala Ser Gln Gly Ala Glu Leu Val Val Phe Pro Glu Leu  
35 40 45

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Thr Leu Thr Thr Phe Phe Pro Arg Thr Trp Phe Glu Glu Gly Asp Phe  
50 55 60

Glu Glu Tyr Phe Asp Lys Ser Met Pro Asn Asp Asp Val Ala Pro Leu  
65 70 75 80

Phe Glu Arg Ala Lys Asp Leu Gly Val Gly Phe Tyr Leu Gly Tyr Ala  
85 90 95

Glu Leu Thr Ser Asp Glu Lys Arg Tyr Asn Thr Ser Ile Leu Val Asn  
100 105 110

Lys His Gly Asp Ile Val Gly Lys Tyr Arg Lys Met His Leu Pro Gly  
115 120 125

His Ala Asp Asn Arg Glu Gly Leu Pro Asn Gln His Leu Glu Lys Lys  
130 135 140

Tyr Phe Arg Glu Gly Asp Leu Gly Phe Gly Val Phe Asp Phe His Gly  
145 150 155 160

Val Gln Val Gly Met Cys Leu Cys Asn Asp Arg Arg Trp Pro Glu Val  
165 170 175

Tyr Arg Ser Leu Ala Leu Gln Gly Ala Glu Leu Val Val Leu Gly Tyr  
180 185 190

Asn Thr Pro Asp Phe Val Pro Gly Trp Gln Glu Glu Pro His Ala Lys  
195 200 205

Met Phe Thr His Leu Leu Ser Leu Gln Ala Gly Ala Tyr Gln Asn Ser  
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Val Phe Val Ala Ala Ala Gly Lys Ser Gly Phe Glu Asp Gly His His  
225 230 235 240

Met Ile Gly Gly Ser Ala Val Ala Ala Pro Ser Gly Glu Ile Leu Ala  
245 250 255

Lys Ala Ala Gly Glu Gly Asp Glu Val Val Val Val Lys Ala Asp Ile  
260 265 270

Asp Met Gly Lys Pro Tyr Lys Glu Ser Val Phe Asp Phe Ala Ala His  
275 280 285

Arg Arg Pro Asp Ala Tyr Gly Ile Ile Ala Glu Arg Lys Gly Arg Gly  
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 <213> *Arthrobacter crystallopoietes*

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 Lys Ile Arg Ala Asp Val Leu Ile Glu Asn Gly Lys Val Ala Ala Val  
 20 25 30  
 ggc atg ctg gac gcc gcg acg ccg gac aca gtt gag cgg gtt gac tgc 144  
 Gly Met Leu Asp Ala Ala Thr Pro Asp Thr Val Glu Arg Val Asp Cys  
 35 40 45  
 gac ggc aaa tac gtc atg ccc ggc ggt atc gac gtt cac acc cac atc 192  
 Asp Gly Lys Tyr Val Met Pro Gly Gly Ile Asp Val His Thr His Ile  
 50 55 60  
 gac tcc ccc ctc atg ggg acc acc acc gcc gat gat ttt gtc agc gga 240  
 Asp Ser Pro Leu Met Gly Thr Thr Thr Ala Asp Asp Phe Val Ser Gly  
 65 70 75 80  
 acg att gca gcc gct acc ggc gga aca acg acc atc gtc gat ttc gga 288  
 Thr Ile Ala Ala Ala Thr Gly Gly Thr Thr Thr Ile Val Asp Phe Gly  
 85 90 95  
 cag cag ctc gcc ggc aag aac ctg ctg gaa tcc gca gac gcg cac cac 336  
 Gln Gln Leu Ala Gly Lys Asn Leu Leu Glu Ser Ala Asp Ala His His  
 100 105 110  
 aaa aag gcg cag ggg aaa tcc gtc att gat tac ggc ttc cat atg tgc 384  
 Lys Lys Ala Gln Gly Lys Ser Val Ile Asp Tyr Gly Phe His Met Cys  
 115 120 125  
 gtg acg aac ctc tat gac aat ttc gat tcc cat atg gca gaa ctg aca 432  
 Val Thr Asn Leu Tyr Asp Asn Phe Asp Ser His Met Ala Glu Leu Thr  
 130 135 140  
 cag gac gga atc tcc agt ttc aag gtc ttc atg gcc tac cgc gga agc 480  
 Gln Asp Gly Ile Ser Ser Phe Lys Val Phe Met Ala Tyr Arg Gly Ser  
 145 150 155 160  
 ctg atg atc aac gac ggc gaa ctg ttc gac atc ctc aag gga gtc ggc 528  
 Leu Met Ile Asn Asp Gly Glu Leu Phe Asp Ile Leu Lys Gly Val Gly  
 165 170 175  
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 Ser Ser Gly Ala Lys Leu Cys Val His Ala Glu Asn Gly Asp Val Ile  
 180 185 190  
 gac agg atc gcc gcc gac ctc tac gcc caa gga aaa acc ggg ccc ggg 624  
 Asp Arg Ile Ala Ala Asp Leu Tyr Ala Gln Gly Lys Thr Gly Pro Gly  
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 acc cac gag atc gca cgc ccg ccg gaa tcg gaa gtc gaa gca gtc agc 672  
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aca Thr	gga Gly	tgg Trp	cca Pro 260	atc Ile	agc Ser	gcc Ala	gaa Glu 265	acg Thr 265	tgc Cys	acc Thr	cac His	tac Tyr	ctg Leu 270	tcg Ser	ctg Leu	816
agc Ser	cgg Arg	gac Asp 275	atc Ile	tac Tyr	gac Asp	cag Gln	ccg Pro 280	gga Gly	ttc Phe	gag Glu	ccg Pro	gcc Ala 285	aaa Lys	gct Ala	gtc Val	864
ctc Leu	aca Thr 290	cca Pro	ccg Pro	ctg Leu	cgc Arg	aca Thr 295	cag Gln	gaa Glu	cac His	cag Gln	gac Asp 300	gcg Ala	ttg Leu	tgg Trp	aga Arg	912
ggc Gly 305	att Ile	aac Asn	acc Thr	ggt Gly	gcg Ala 310	ctc Leu	agc Ser	gtc Val	gtc Val	agt Ser 315	tcc Ser	gac Asp	cac His	tgc Cys	ccc Pro 320	960
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gga Gly 385	aca Thr	att Ile	gca Ala	ccg Pro	ggc Gly 390	tcc Ser	gat Asp	gca Ala	gac Asp	atc Ile 395	atc Ile	gtg Val	gtc Val	gac Asp	ccc Pro 400	1200
aac Asn	gga Gly	aca Thr	acc Thr	ctc Leu 405	atc Ile	agt Ser	gcc Ala	gac Asp	acc Thr 410	caa Gln	aaa Lys	caa Gln	aac Asn	atg Met 415	gac Asp	1248
tac Tyr	acg Thr	ctg Leu	ttc Phe 420	gaa Glu	ggc Gly	ttc Phe	aaa Lys	atc Ile 425	cgt Arg	tgc Cys	tcc Ser	atc Ile	gac Asp 430	cag Gln	gtg Val	1296
ttc Phe	tcg Ser	cgt Arg 435	ggc Gly	gac Asp	ctg Leu	atc Ile	agc Ser 440	gtc Val	aaa Lys	ggc Gly	gaa Glu	tat Tyr 445	gtc Val	ggc Gly	acc Thr	1344
cgc Arg	ggc Gly 450	cgc Arg	ggc Gly	gaa Glu	ttc Phe	atc Ile 455	aag Lys	cgg Arg	agc Ser	gct Ala	tgg Trp 460	agc Ser	cac His	ccg Pro	cag Gln	1392
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&lt;213&gt; Arthrobacter crystallopoietes

&lt;400&gt; 4

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35 40 45Asp Gly Lys Tyr Val Met Pro Gly Gly Ile Asp Val His Thr His Ile  
50 55 60Asp Ser Pro Leu Met Gly Thr Thr Thr Ala Asp Asp Phe Val Ser Gly  
65 70 75 80Thr Ile Ala Ala Ala Thr Gly Gly Thr Thr Thr Ile Val Asp Phe Gly  
85 90 95Gln Gln Leu Ala Gly Lys Asn Leu Leu Glu Ser Ala Asp Ala His His  
100 105 110Lys Lys Ala Gln Gly Lys Ser Val Ile Asp Tyr Gly Phe His Met Cys  
115 120 125Val Thr Asn Leu Tyr Asp Asn Phe Asp Ser His Met Ala Glu Leu Thr  
130 135 140Gln Asp Gly Ile Ser Ser Phe Lys Val Phe Met Ala Tyr Arg Gly Ser  
145 150 155 160Leu Met Ile Asn Asp Gly Glu Leu Phe Asp Ile Leu Lys Gly Val Gly  
165 170 175Ser Ser Gly Ala Lys Leu Cys Val His Ala Glu Asn Gly Asp Val Ile  
180 185 190Asp Arg Ile Ala Ala Asp Leu Tyr Ala Gln Gly Lys Thr Gly Pro Gly  
195 200 205Thr His Glu Ile Ala Arg Pro Pro Glu Ser Glu Val Glu Ala Val Ser  
210 215 220Arg Ala Ile Lys Ile Ser Arg Met Ala Glu Val Pro Leu Tyr Phe Val  
225 230 235 240His Leu Ser Thr Gln Gly Ala Val Glu Glu Val Ala Ala Ala Gln Met  
245 250 255

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Thr Gly Trp Pro Ile Ser Ala Glu Thr Cys Thr His Tyr Leu Ser Leu  
260 265 270

Ser Arg Asp Ile Tyr Asp Gln Pro Gly Phe Glu Pro Ala Lys Ala Val  
275 280 285

Leu Thr Pro Pro Leu Arg Thr Gln Glu His Gln Asp Ala Leu Trp Arg  
290 295 300

Gly Ile Asn Thr Gly Ala Leu Ser Val Val Ser Ser Asp His Cys Pro  
305 310 315 320

Phe Cys Phe Glu Glu Lys Gln Arg Met Gly Ala Asp Asp Phe Arg Gln  
325 330 335

Ile Pro Asn Gly Gly Pro Gly Val Glu His Arg Met Leu Val Met Tyr  
340 345 350

Glu Thr Gly Val Ala Glu Gly Lys Met Thr Ile Glu Lys Phe Val Glu  
355 360 365

Val Thr Ala Glu Asn Pro Ala Lys Gln Phe Asp Met Tyr Pro Lys Lys  
370 375 380

Gly Thr Ile Ala Pro Gly Ser Asp Ala Asp Ile Ile Val Val Asp Pro  
385 390 395 400

Asn Gly Thr Thr Leu Ile Ser Ala Asp Thr Gln Lys Gln Asn Met Asp  
405 410 415

Tyr Thr Leu Phe Glu Gly Phe Lys Ile Arg Cys Ser Ile Asp Gln Val  
420 425 430

Phe Ser Arg Gly Asp Leu Ile Ser Val Lys Gly Glu Tyr Val Gly Thr  
435 440 445

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Phe Glu Lys  
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60

70

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